Supplementary data

Molecular perception of interactions between bis(7)tacrine and cystamine-tacrine dimer with cholinesterases as the promising proposed agents for the treatment of Alzheimer's disease

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Figure S1. RMSD plot of both enzymes backbones in their two different protonation states; (a) AChE enzyme, (b) BChE enzyme; The blue and red curves represent RMSD plot of AChE backbone when Glu199 and Glu445 of it are considered uncharged and charged, respectively, The magenta and green curves represent RMSD plot of BChE backbone when Glu197 and Glu442 of it are considered uncharged and charged, respectively.

Figure S2. RMSF of the selected residues of both enzymes in their two protonation states; (a) AChE enzyme, (b) BChE enzyme; The blue and red curves represent RMSD plot of AChE backbone when Glu199 and Glu445 of it are considered uncharged and charged, respectively. The magenta and green curves represent RMSD plot of BChE backbone when Glu197 and Glu442 of it are considered uncharged and charged, respectively.

Figure S3. Evaluation of pivotal hydrogen bonds in the catalytic triad; (a): The distance between oxygen atom from the carbonyl group of Glu327 and N^{γ} of His440 imidazole ring, (b): The distance between O^{γ} of Ser200 and $N^{\epsilon 2}$ of His440, (c): The distance between O^{γ} of Ser198 and $N^{\epsilon 2}$ of His438, (d): The distance between oxygen from the carbonyl group of Glu325 and delta nitrogen of His438 imidazole ring; The blue and red curves represent RMSD plot of AChE backbone when Glu199 and Glu445 of it are considered uncharged and charged, respectively. The magenta and green curves represent RMSD plot of BChE backbone when Glu197 and Glu442 of it are considered uncharged and charged, respectively.

Figure S4. Two-dimensional representations of the observed interactions between both enzymes and all the ligands; residues in a green frame: van der Waals interaction, residues in a magenta frame: electrostatic interaction, cyan small rectangles: water molecules, Orange lines: π - π interaction, blue dashed line with arrow at H-bond acceptor: hydrogen bond with amino acid side-chain, green dashed line with arrow at H-bond acceptor: hydrogen bond with amino acid main chain, black dashed line with arrow at H-bond acceptor: hydrogen bond with non-amino acid; (a) AChE-bis(7)tacrine, (b) AChE-cystaminetacrine dimer, (c) AChE-tacrine, (d) BChE-bis(7)tacrine, (e) BChE-cystaminetacrine dimer, (f) BChE-tacrine.

Figure S5. Solvent accessible surface area (SASA) of the proteins, (a) AChE in complex with bis(7)tacrine (violet), cystamine-tacrine dimer (green), and tacrine (orange), (b) BChE in complex with bis(7)tacrine (blue), cystamine-tacrine dimer (forest green), and tacrine (magenta).

Figure S6. RMSF plots of both enzymes Ω loop; (a) AChE enzyme, and (b) BChE enzyme.